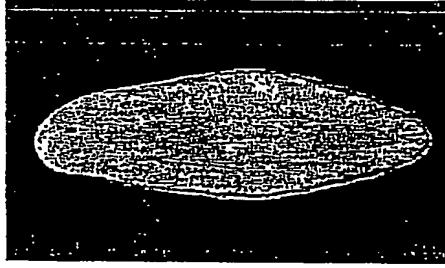


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EST ID: D21.6.Contig  
 Accession: AY062374  
 cDNA Sequence: CTTCTGCAAGGTCCACAGTTACCATAACAAATCGAGTCCTGCACTAAAGGAATATGAAA  
 TGACACAAATCCTACAATTTCTGGAGCACCTATGGGGGATCACTTAAATTCTAGCA  
 ATGTGTCTTCTGCTGTAGAGGGCCGAGAAAAGAGAGAAAATGCNAGATCTAATG  
 AAAGGCTAGCTAATTATATTGAAAAGTAAGATTCTAGAAGCTCNAACAAAAGATTAA  
 CAAATGAATTGAATACTGTTACGTGAAAGATGGGTNAAGAAGCTGAAAGGATACGAGCTT  
 TATATGAGATTGAAATGGATCAATTGAAAAAGTTATTAGACGAAGCTGAAGCTGCTAGAT

Category: Cytoskeletal/Structural  
 Subcategory: intermediate filaments  
 In Situ: 

Query= D21.6.Contig (1828 letters) Database: nr 775,385 sequences; 246,391,666 total letters Searching done

Score (bits)	E Value
Sequences producing significant alignments:	
dbj BAB64909.1  (AB056671) intermediate filament b [Dugesia...	471 e-131
emb CAA68255.1  (X99996) intermediate filament protein [Lin...	412 e-114
emb CAB38180.1  (AJ004937) cytoplasmic intermediate filamen...	411 e-114
emb CAA69027.1  (Y07747) IF protein [Lineus viridis]	397 e-109
gb AAD29248.1 AF101065 1 (AF101065) intermediate filament g...	392 e-108

>dbj|BAB64909.1| (AB056871) intermediate filament b [Dugesia japonica]  
 >dbj|BAB64910.1| (AB056872) intermediate filament b [Dugesia japonica]  
 Length = 610

Score = 471 bits (1211), Expect = e-131  
 Identities = 244/567 (43%), Positives = 365/567 (64%), Gaps = 10/567 (1%)  
 Frame = +3

Query: 27 NXSSPAVKEYMRQSYNFGAPMGGSVQIHSNVSSAVEGREREKREMXDNLNERLANYIEK 206  
 N+++ +++ EM++SY S P S +HS V++ +GRE+EK E+ +LN+R ANYI+K  
 Sbjct: 45 NQNASSIRTIEKKSYGVSATPGATSNIVHSGVNNLMNGREKEKNEQELNDRFANYIDK 104

Query: 207 VRFLEAXNKRLTNEALTRERHGXEAEIRALYEIEMDQLKKLLDEAFARSELLPKINK 366  
 VR LE NKRLT+ELN L+++HG E RI+ALY+ +M QL++ LD+AEA+++L KIN  
 Sbjct: 105 VRSLEDENKRLTDELNDLKQWGNETARIKALYDSDMSQLRRSLDQAEASKAQLEMKINT 164

FIG. 2

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Cell defense (32)  CELL-cell communication (136)  
 carrier proteins (2)  adhesion (27)  
 DNA repair (2)  extracellular matrix (33)  
 immunology (?) (0)  hormone/growth factors/activators (19)  
 stress response (26)  other membrane proteins (34)  
 receptors (24)

Cytoskeletal/Structural (139)  DNA Replication/Modification (130)  
 intermediate filaments (10)  apoptosis (31)  
 microfilaments (47)  cell cycle/division (56)  
 microtubules (35)  chromosome/nuclear structure (21)  
 others (27)  DNA synthesis (22)

thick/thin filaments (20)

General Metabolism (228)  Intracellular Signaling (211)  
 amino acids (25)  channels/transporters (39)  
 lipids (66)  effectors/modulators (39)  
 nucleotides (18)  protein kinases (44)  
 other enzymes/cofactors (56)  protein phosphatases (16)  
 sugar/glycolysis (65)  transduction (37)

Mitochondria (72)  No Match (1281)

Protein Metabolism (175)  RNA Metabolism (137)  
 degradation (63)  RNA binding (17)  
 folding (23)  RNA polymerases (2)  
 post-translational modification (10)  RNA processing (44)  
 ribosomal components (39)  transcription factors (77)

translation factors (32)

tRNA synthesis (10)

Secretary Pathways (88)  Unknown Function (357)  
 endoplasmic reticulum (27)  invertebrates (175)  
 golgi (28)  plants (12)  
 nuclear components (33)  Prokaryotes (9)  
 vertebrates (159)  
 yeast (4)

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Please check off a Category and/or Sub-categories to search, or type in an Accession Number:

Search via Accession Number:

**Cell defense (32)**

carrier proteins (2)

DNA repair (2)

immunology (?) (0)

stress response (26)

**Cytoskeletal/Structural (139)**

intermediate filaments (10)

microfilaments (47)

microtubules (35)

others (27)

thick/thin filaments (20)

**General Metabolism (228)**

amino acids (25)

lipids (66)

nucleotides (18)

other enzymes/cofactors (56)

sugar/glycolysis (65)

**Mitochondria (72)**

**Protein Metabolism (175)**

degradation (63)

folding (23)

post-translational modification (10)

ribosomal components (39)

translation factors (32)

tRNA synthesis (10)

**Secretary Pathways (88)**

endoplasmic reticulum (27)

golgi (28)

vesicular components (33)

**CELL-cell communication (136)**

adhesion (27)

extracellular matrix (33)

hormone/growth factors/activators (19)

other membrane proteins (34)

receptors (24)

**DNA Replication/Modification (130)**

apoptosis (31)

cell cycle/division (56)

chromosome/nuclear structure (21)

DNA synthesis (22)

**Intracellular Signaling (211)**

channels/transporters (39)

effectors/modulators (39)

protein kinases (44)

protein phosphatases (16)

transduction (37)

**No Match (1281)**

**RNA Metabolism (137)**

RNA binding (17)

RNA polymerases (2)

RNA processing (44)

transcription factors (77)

**Unknown Function (357)**

invertebrates (175)

plants (12)

Prokaryotes (9)

vertebrates (159)

yeast (4)

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FIGURE 2

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		Your search produced 10 results		
		EST ID Accession Number	Description	Category Sub-category
<a href="#">Home</a>	<a href="#">Search</a>	D.21.6.Catig AV068374	(AB056871) intermediate filament b [Dugesia-jaboricu]	Cytoskeletal/Structural * intermediate filaments
<a href="#">SmedDb</a>	<a href="#">Search VA</a>	<a href="#">More Info</a>		<a href="#">view InSitu</a>
<a href="#">Blast</a>	<a href="#">Publications</a>	H.102.6e AV068720	(AF339450) hilarin [Hrudo medicinalis]	Cytoskeletal/Structural * intermediate filaments
<a href="#">Regeneration</a>	<a href="#">In the News</a>	<a href="#">More Info</a>		<a href="#">(none available)</a>
<a href="#">Lab Members</a>	<a href="#">Contact Us</a>	H.102.6e(13) AV068721	(AF339450) hilarin [Hrudo medicinalis]	Cytoskeletal/Structural * intermediate filaments
<a href="#">Credits</a>	<a href="#">Other Info</a>	<a href="#">More Info</a>		<a href="#">(none available)</a>
		H.106.2E AV067086	(AB056871) intermediate filament b [Dugesia-jaboricu]	Cytoskeletal/Structural * intermediate filaments
		<a href="#">More Info</a>		<a href="#">(none available)</a>
		H.12.11A AV067087	(AB056871) intermediate filament b [Dugesia-jaboricu]	Cytoskeletal/Structural * intermediate filaments
		<a href="#">More Info</a>		<a href="#">view InSitu</a>
		H.24.6b AV068722	(M07747) IF protein [Linus vitidis]	Cytoskeletal/Structural * intermediate filaments
		<a href="#">More Info</a>		<a href="#">(none available)</a>

FIG. 4

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Blast Search

Search name

Blast Parameters  
 Search type  
 blastn   
 Expected Value

Sequence

```
CTCTGCAAGGTCACAGTTAACAAATCGAGTCCTGCAGTTAACAAATATGAAA
TGAGACAATCTTACAATTTTCTGGAGCACCTATGGGGGATCAGTTCAATTCAATAGA
ATGTCCTCTGGCTAGAGGGGGAGAAAAGAGAAAATGCNAGATCTTAATG
AAAGCTAGCTAAATTATGAAAAGGTAAGTTCTAGAACCTCNAAAACAAAAGATTAA
```

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FIG. 5A

BLASTM 2.1.2 [Nov-13-2000]

## Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandra A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query TEST

(1828 letters)

Database: Smed

3890 sequences; 2,526,228 total letters

Sequences producing significant alignments:	Score	E
	(bits)	Value
ref Smed4531 D21.6.Contig	2495	0.0
ref Smed3960 HB.24.7g	36	0.057
ref Smed2705 H.97.6h	36	0.057
ref Smed2761 H.9.7f	34	0.23
ref Smed3456 H.111.3b	34	0.23
ref Smed2084 H.83.9h	34	0.23
ref Smed1429 H.44.7g	34	0.23
ref Smed3687 H.44.2c(T3)	32	0.89
ref Smed3653 H.86.9d	32	0.89
ref Smed3328 H.2.7a	32	0.89
ref Smed3058 H.50.4e	32	0.89
ref Smed1991 H.57.2c	32	0.89
ref Smed1880 H.59.12c	32	0.89
ref Smed448 H.17.3e	30	0.89
ref Smed4748 HB.9.4f	30	3.5
ref Smed4734 H.67.11d(T3)	30	3.5
ref Smed4692 H.73.7c	30	3.5
ref Smed4308 HB.35.4e	30	3.5
ref Smed4263 HB.29.8e	30	3.5
ref Smed4244 HB.22.6a	30	3.5
ref Smed3859 H.98.8c(T3)	30	3.5

FIG. 5B-1

ref   Smed3806   H.29.9d(T3)	30	3.5
ref   Smed3670   H.40.7b(T3)	30	3.5
ref   Smed3284   H.29.10f	30	3.5
ref   Smed3224   H.30.1e	30	3.5
ref   Smed3143   H.38.10f	30	3.5
ref   Smed2842   H.9.4b	30	3.5
ref   Smed2143   H.35.6a(T3)	30	3.5
ref   Smed1718   H.49.1d(T3)	30	3.5
ref   Smed1992   H.6.1e	30	3.5
ref   Smed1332   H.104.5d	30	3.5
ref   Smed1208   H.83.7g	30	3.5
ref   Smed1167   H.24.6d	30	3.5
ref   Smed476   H.92.5f	30	3.5
ref   Smed464   H.69.2a	30	3.5

>ref | Smed4531 | D21.6.Contig  
Length = 1828

Score = 2495 bits (1258), Expect = 0.0

Identities = 1281/1281 (100%)

Strand = Plus / Plus

Query: 1 cttctgcaaggccacagttaccat taacaaatcgagtcctgcagtaaaggaaatatgaaa 60

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 1 cttctgcaaggccacagttaccat taacaaatcgagtcctgcagtaaaggaaatatgaaa 60

Query: 61 tgagacaatccatcaattttctggagcacctatgggggatcaggtaaaattcatagca 120

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 61 tgagacaatccatcaattttctggagcacctatgggggatcaggtaaaattcatagca 120

FIG.5B-2

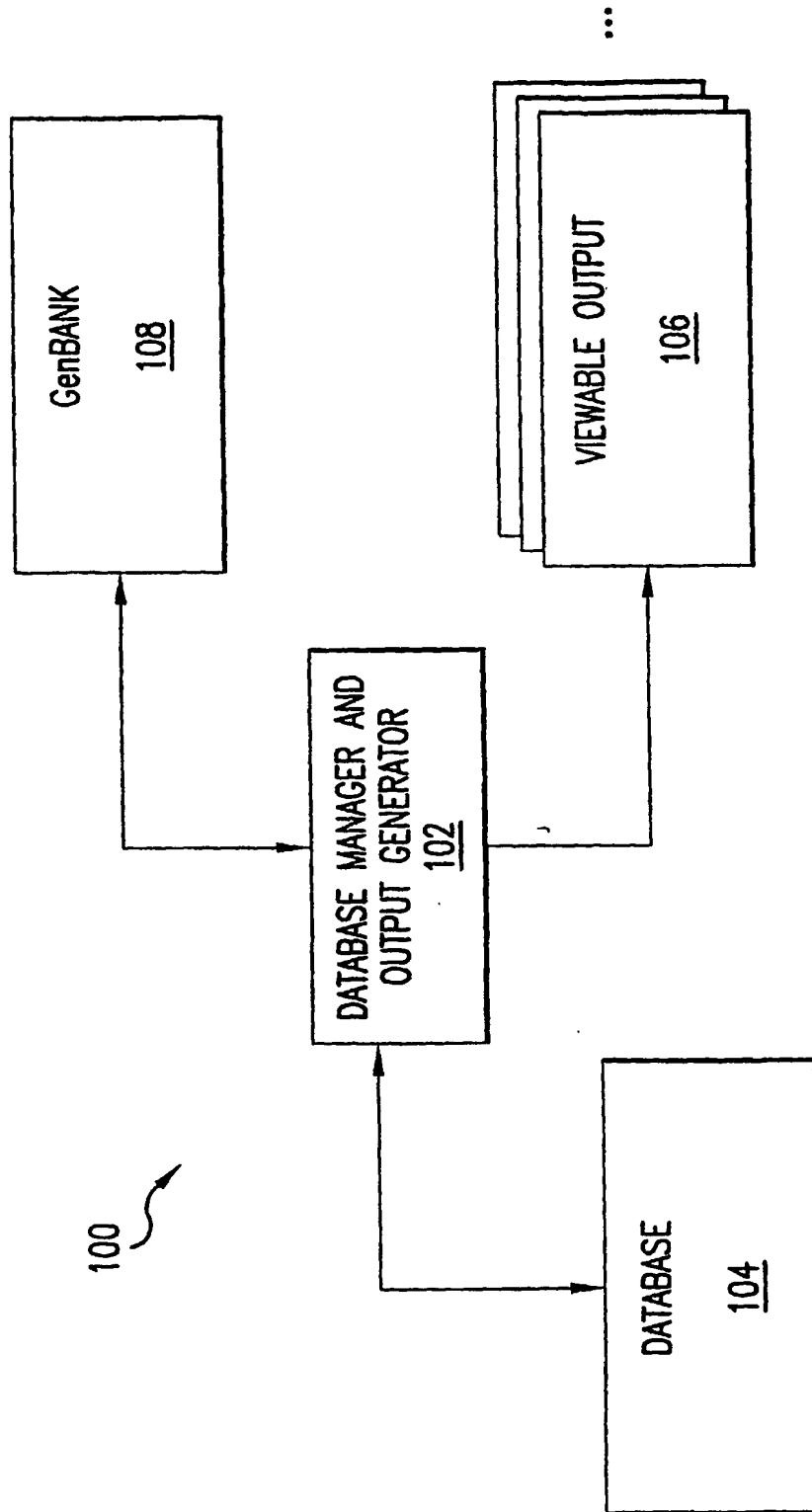


FIG. 6

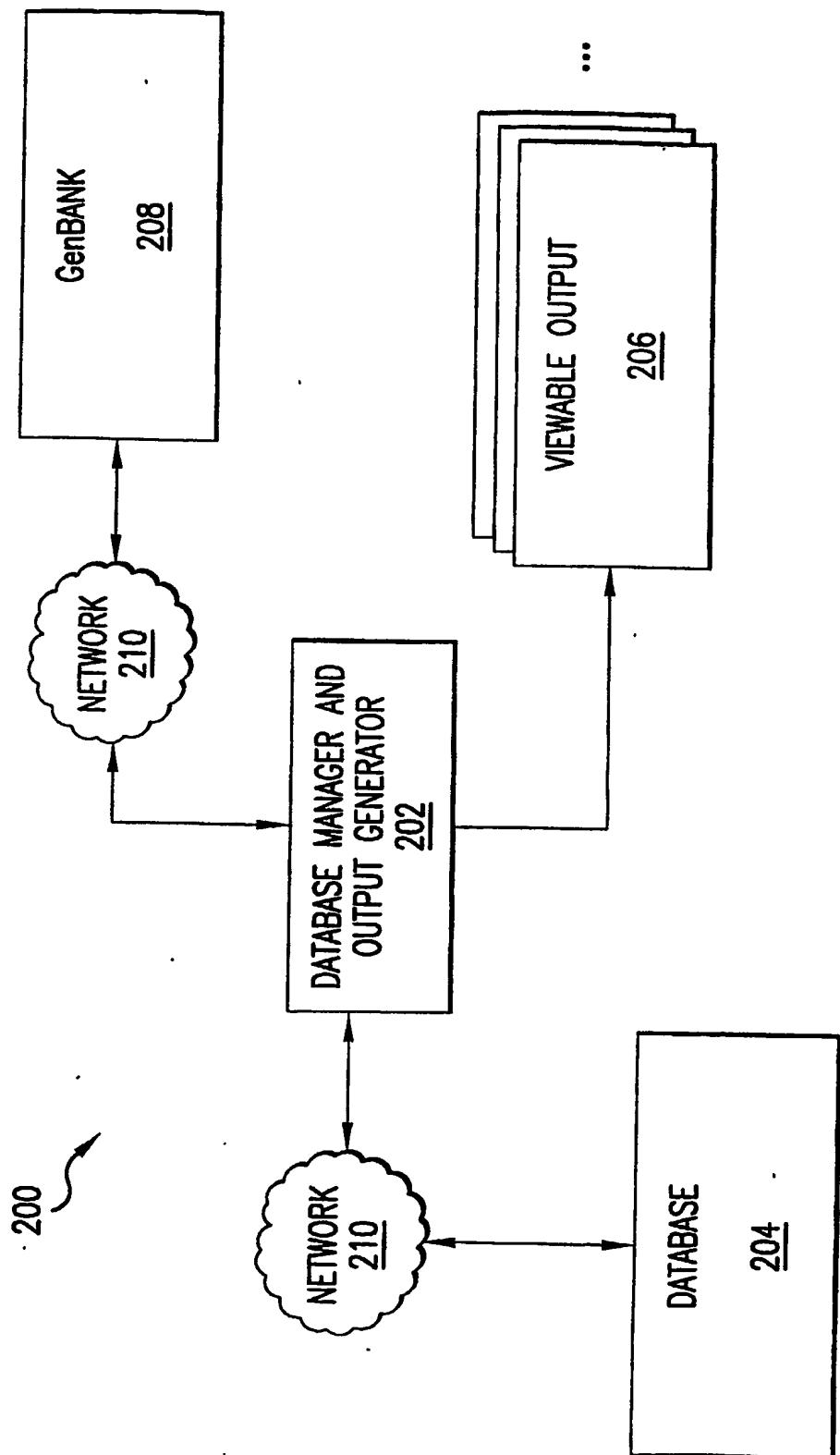


FIG.7

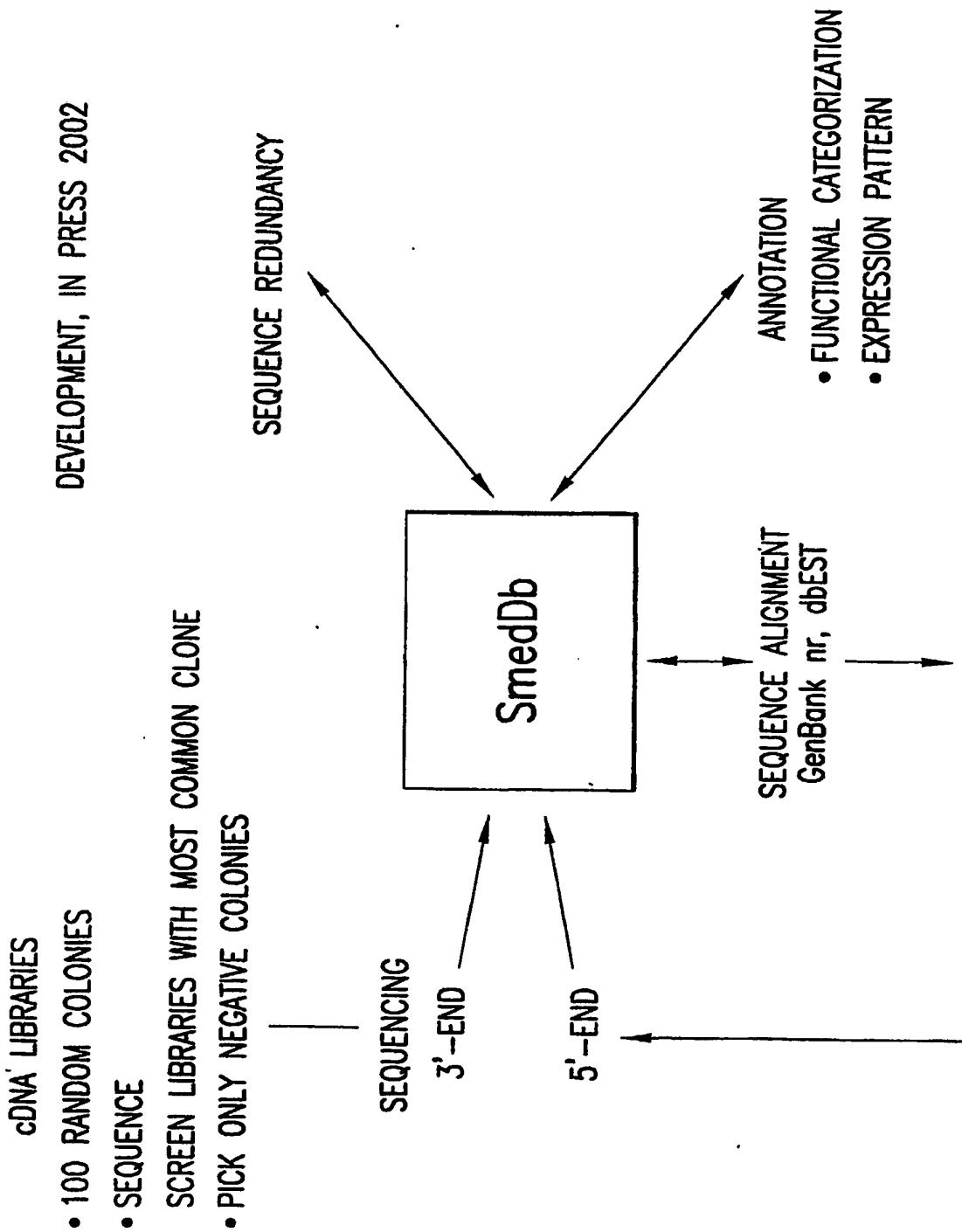


FIG. 8

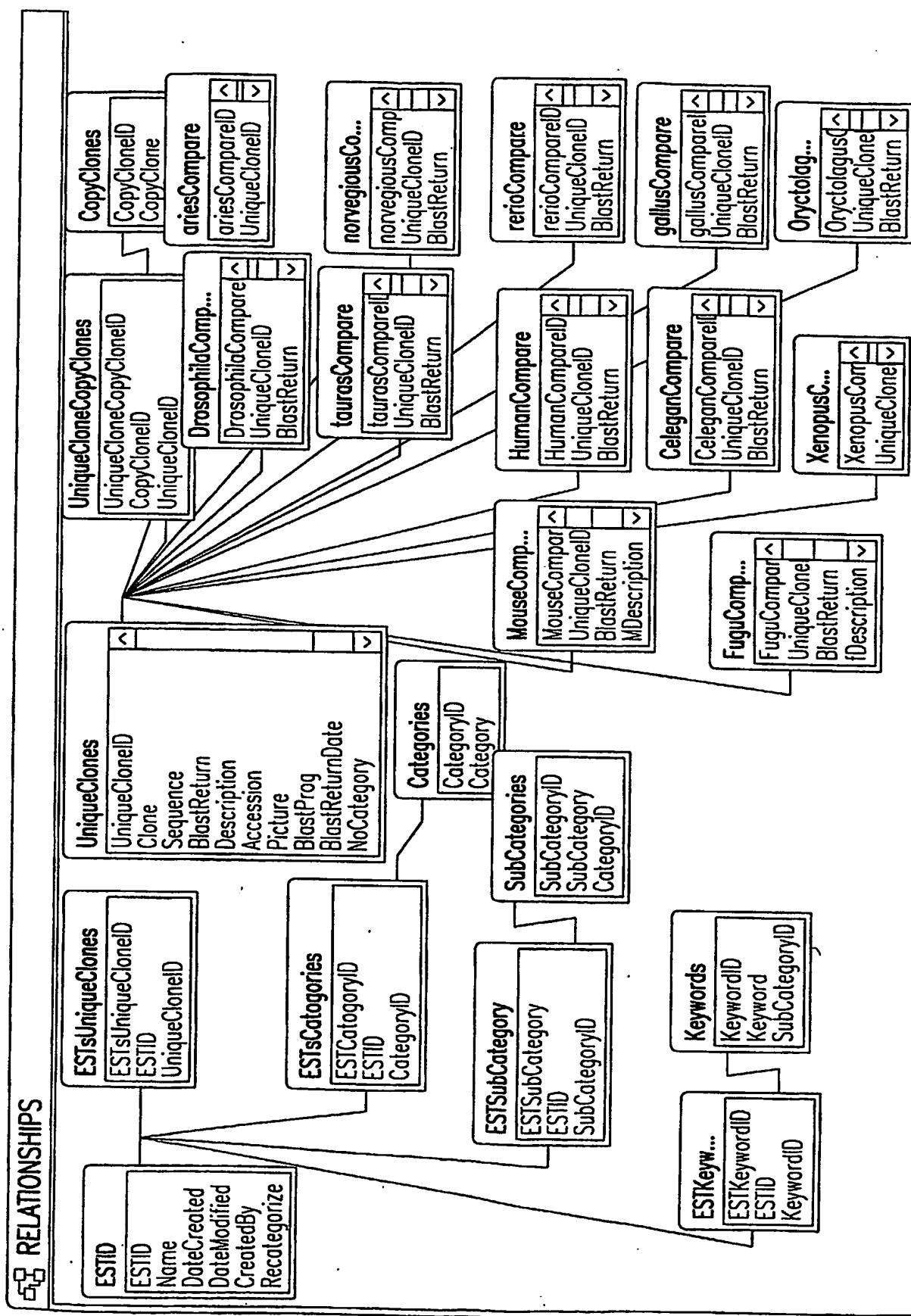


FIG. 9

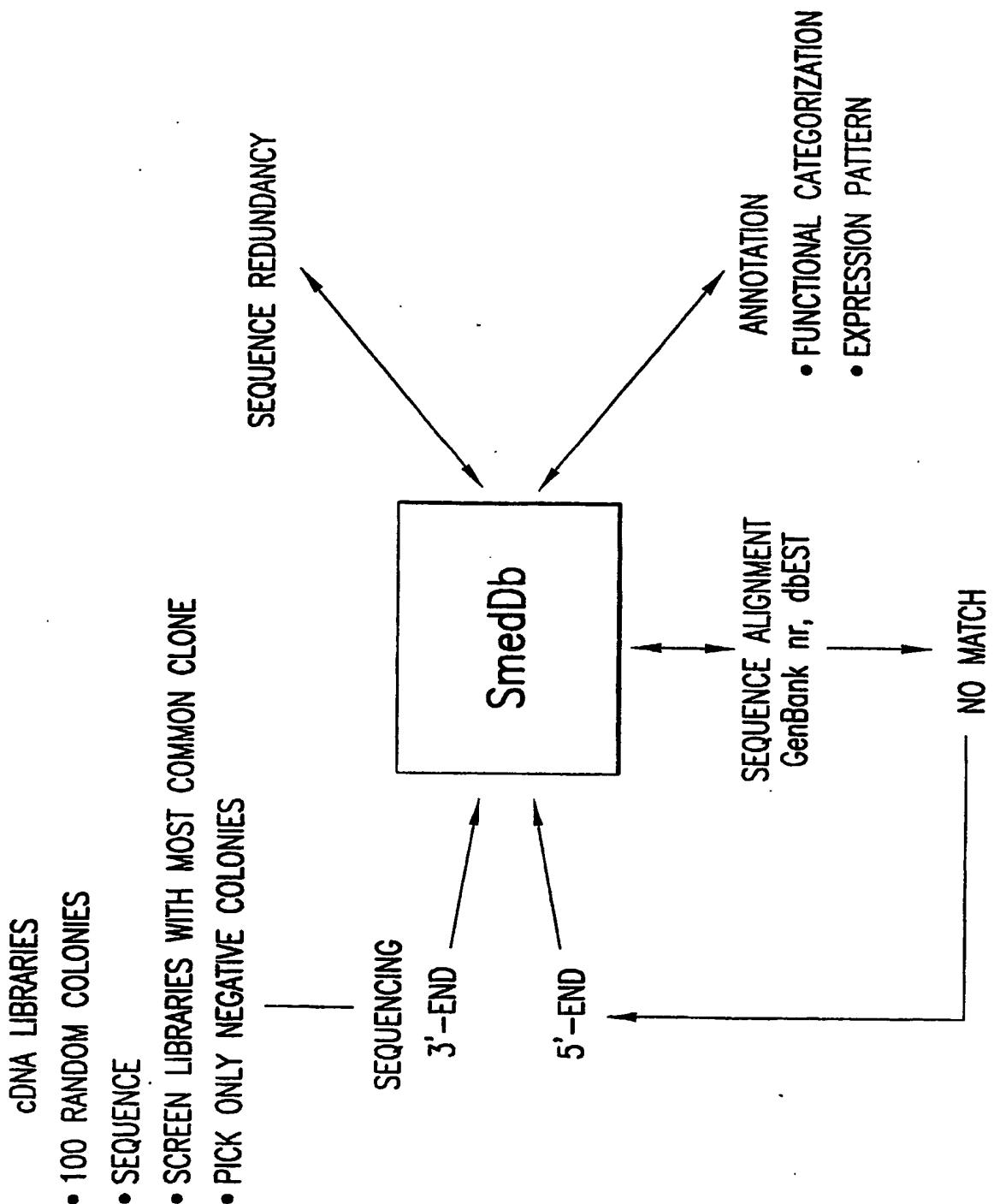


FIG. 10A

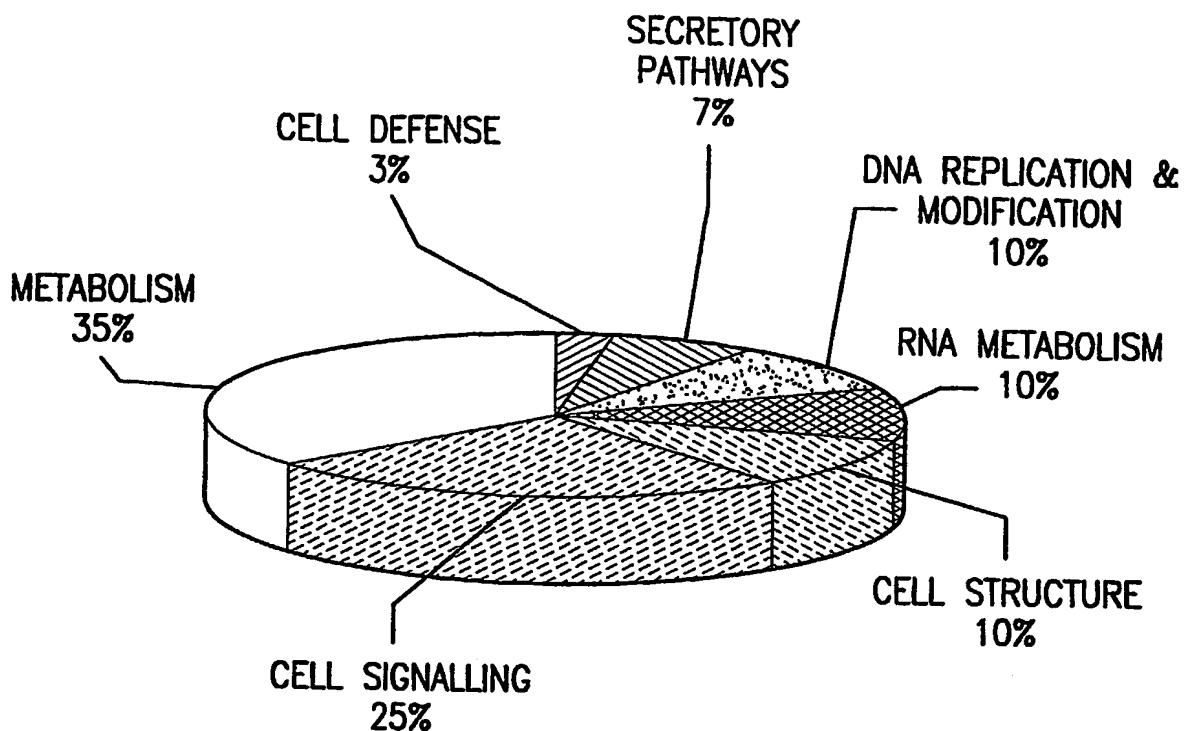


FIG. 10B

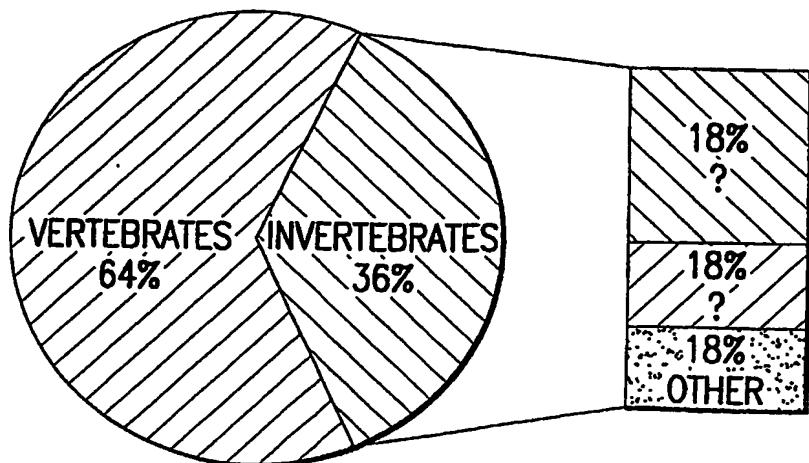


FIG. 10C

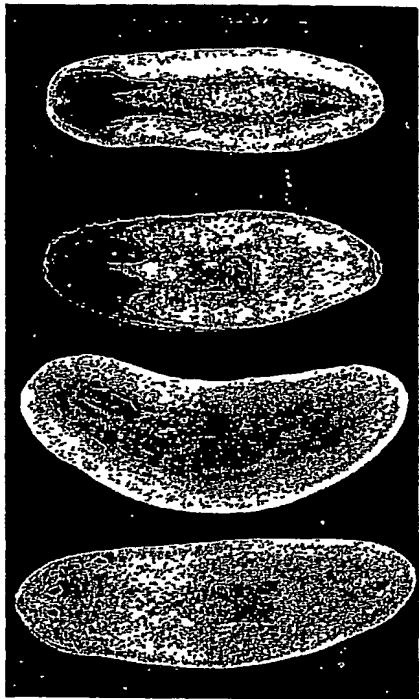


FIG.11A

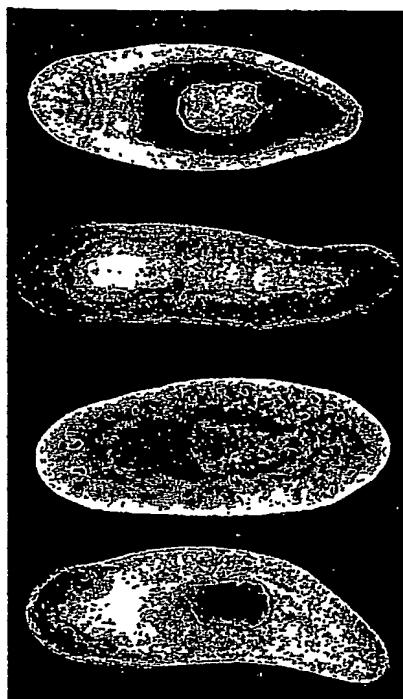


FIG.11B

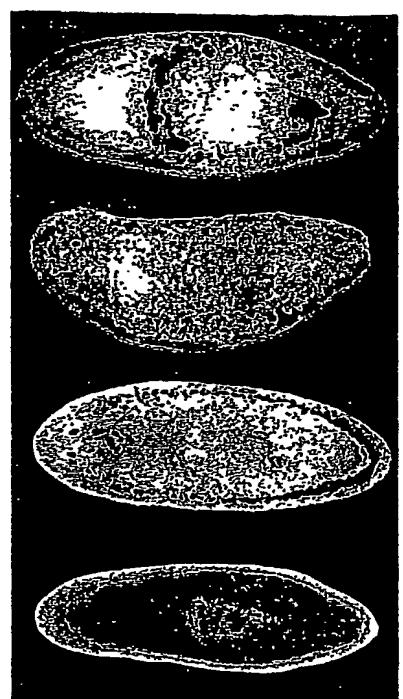


FIG.11C

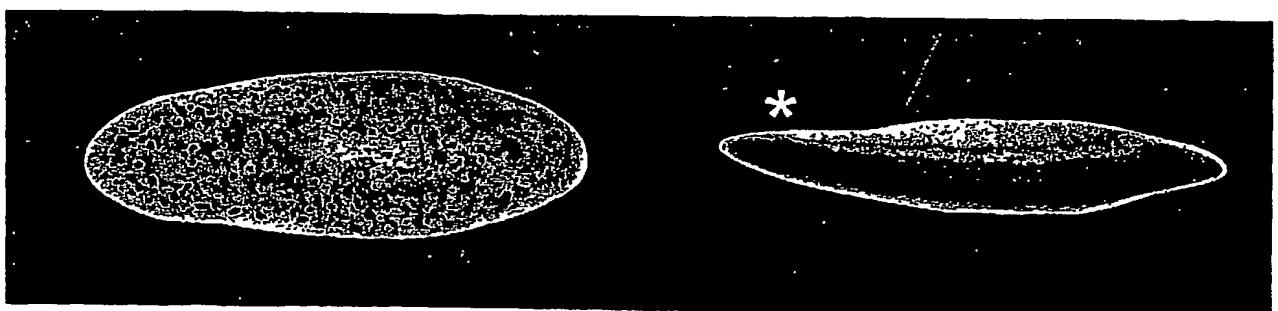


FIG.11D

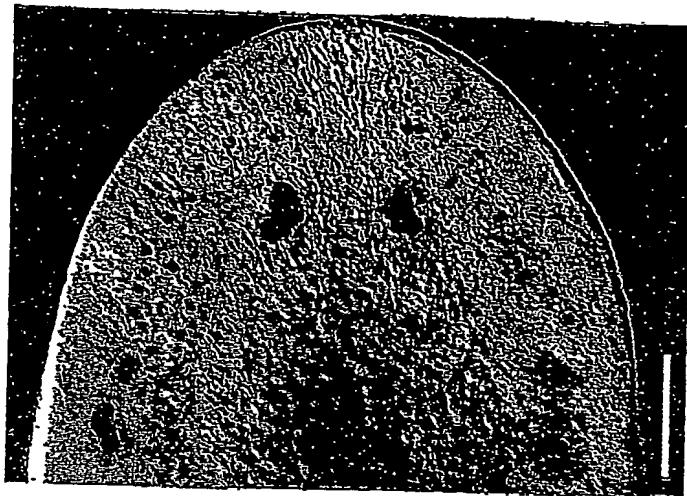


FIG. 12A

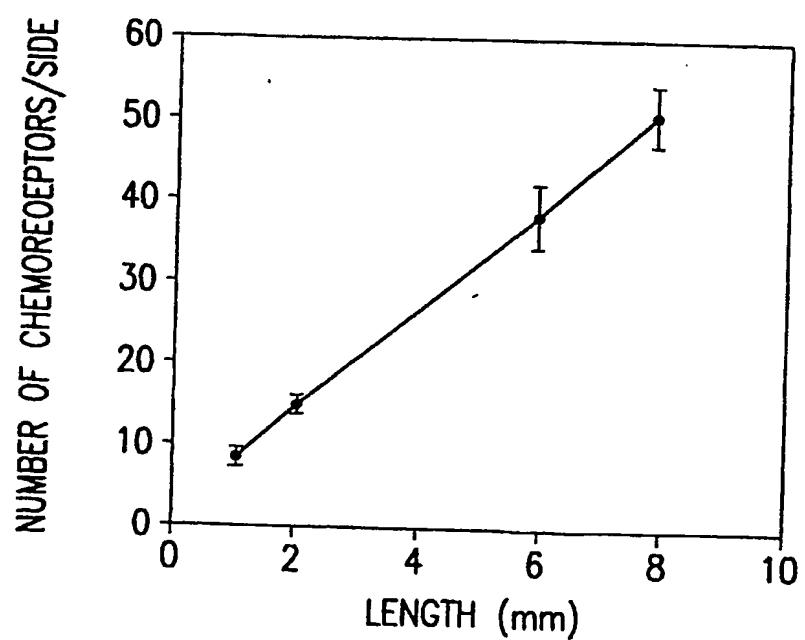


FIG. 12B

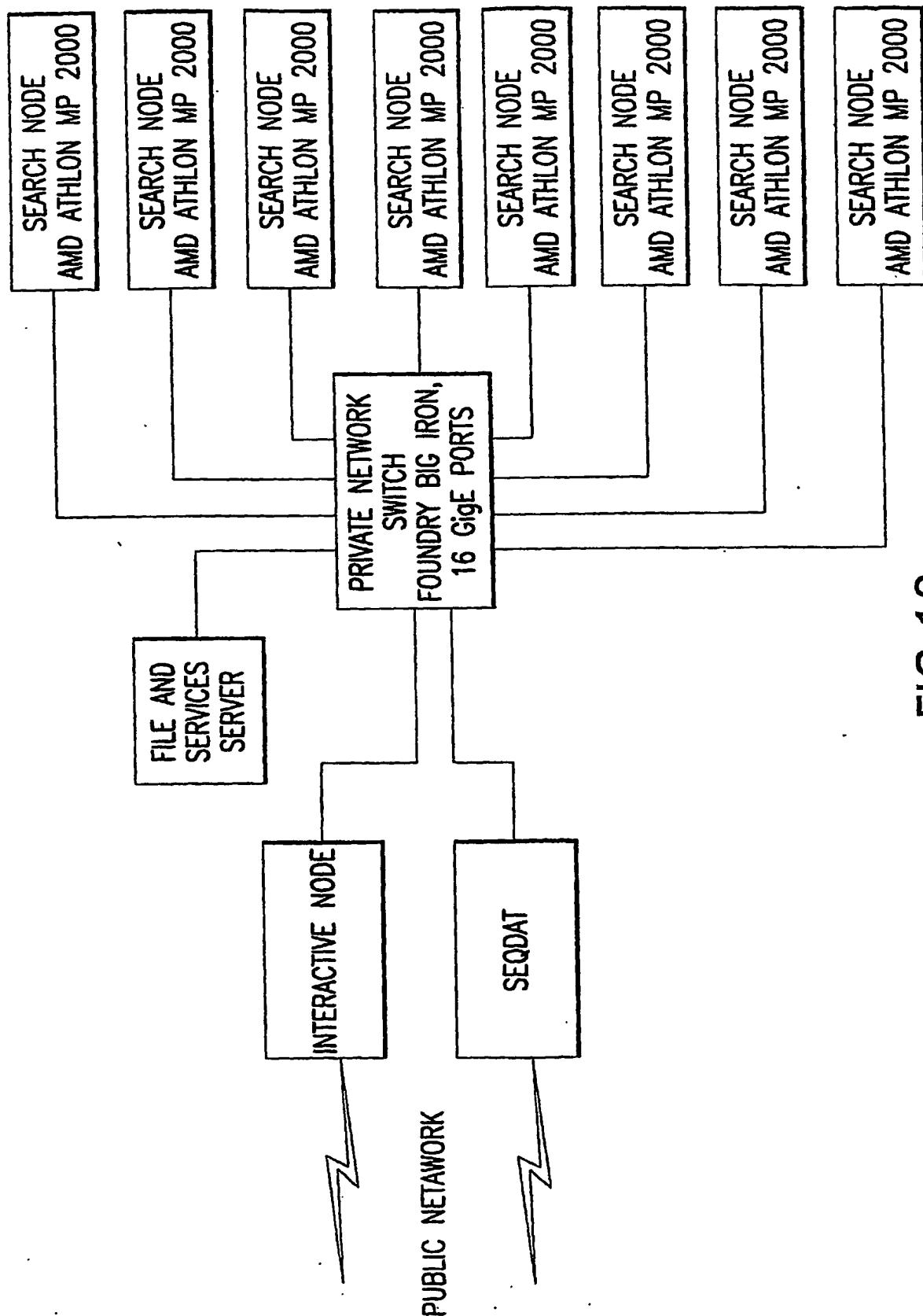


FIG. 13

```
#!/usr/sbin/perl
#
#check if this is a first time search on the input files
#
print "Is this a first time search on datafiles in \$HOME/newsearch (reply yes or no): ";
chomp($flag1 = <STDIN>);

if ($flag1 eq 'yes') {
    $direct = newsearch;
}
#
# if not a first time search
#
if ($flag1 eq 'no') {
    $direct = search;
}
#
#check if new db available - if no then exit
```

FIG. 14A

```

#
$max = @dirs[0];
foreach $n (@dirs) {
    if ($n gt $max)
        { $max = $n; }
}
#
# Now, $max is the lastest date-coded directory
#
$Dir_ID = $max;

$date_last = qx (grep Posted /uufs/inscc.utah.edu/common/home/planaria/$direct/$Dir_ID/1x12.htm | uniq | cut -d "
" -f 8,9,10);
#
#Again change format
# Turn date_last into something useful
#
($m, $d, $y) = split(/ ,/, $date_last);
if ($m eq 'Jan')
    { $month = '01'; }
if ($m eq 'Feb')
    { $month = '02'; }
if ($m eq 'Mar')
    { $month = '03'; }
if ($m eq 'Apr')
    { $month = '04'; }
if ($m eq 'May')
    { $month = '05'; }
if ($m eq 'Jun')
    { $month = '06'; }
if ($m eq 'Jul')
    { $month = '07'; }
if ($m eq 'Aug')
    { $month = '08'; }
if ($m eq 'Sep')
    { $month = '09'; }
if ($m eq 'Oct')
    { $month = '10'; }
if ($m eq 'Nov')
    { $month = '11'; }
if ($m eq 'Dec')
    { $month = '12'; }

$d =~ s/://;
if ($d < 10)
    { $d = '0' . $d; }

chomp ($y);

$date_last_useful = "$y-$month-$d";
print "Date of last database: ", $date_db_useful, "\n";

print "Date of last search db: ", $date_last_useful, "\n";
#
#Compare two dates-if first not later than second exit with message
#

```

FIG. 14 (Cont'd)

```

if (date db useful 1e $date_last_useful)
{die "No database update_since last search. Try again tomorrow as updates are checked for nightly\n";}
}

#check if both searches or only first to be done
#
print "Do you want to do the first search only (enter 1) or fist search and tblastx search (enter 2): ";
chomp($flag = <STDIN>);
print "The information that follows are the jobids for the batch jobs submitted to complete the search. \n";
print "\n";

#do first stage of search
#
#figure out how many nodes are free to use for search
#
$busy = qx(showq|grep Nodes|cut -d " " -f26);
$active = qx(showq|grep Nodes|cut -d " " -f31);
$nodes = $active - $busy;
if ($nodes == 0)
{$nodes = 1;}
print "NODE TO BE USED: \"$nodes,\" \n";

#make necessary directory for output of search
#
($SDAY, $MONTH, $YEAR) = (localtime)[3,4,5];
$MONTH++;
if ($MONTH < 10)
{$MONTH = '0' . $MONTH;}
if ($SDAY < 10)
{$SDAY = '0' . $SDAY; }


```

```

$YEARS = $YEAR + 1900;
if ($flag eq 1)
{system("mkdir -p \$HOME/$direct/$YEARS-$MONTH-$DAY");}
else
{system("mkdir -p \$HOME/$direct/$YEARS-$MONTH-$DAY/TBLASTX");}
#
#set up scripts for first search
#
$source = "$ENV{HOME}/$direct/searchlist.in";
open(IN, "<$source");
@line = <IN>;
foreach (@line)
{chomp;}
#
#Write out PBS header to each of the SCRIPT files being written
#
foreach (1..$nodes){
  $name = "#ENV{HOME}/$direct/SCRIPT-S_";
  open ($name, ">$name");
  print $name ("#PBS -S /bin/csh\n");
  print $name ("#PBS -q sequence\n");
  print $name ("#PBS -W qos=2\n");
  print $name ("#PBS -l walltime=500:00:00,nodes=1:ppn=2\n");
  print $name ("#PBS -N Blast", $_, "\n");
  print $name ("#PBS -e blast", $_, ".stderr\n");
  print $name ("#PBS -o blast", $_, ".stdout\n");
}

```

```

print $name ("setenv BLAST_CLI_HOME /uufs/sequence/sys/pkg/blast/std\n");
print $name ("setenv BLAST_DB /scratch/local/sofia/db\n");
print $name ("setenv WORKDIR \$HOME/$direct\n");
print $name ("cd \$WORKDIR/$YEARS,$MONTH,$DAY,\n");
print $name ("ln -s \$BLAST_CLI_HOME/.ncbirc .ncbirc\n");
print $name ("rm -r /scratch/local/sofia/db\n");
print $name ("mkdir -p /scratch/local/sofia/db\n");
print $name ("cp /uufs/sequence/sys/pkg/blast_db/std/nr.* /scratch/local/sofia/db/\n");
print $name ("cp /uufs/sequence/sys/pkg/blast_db/std/nt.* /scratch/local/sofia/db/\n");
print $name ("cp /uufs/sequence/sys/pkg/blast_db/std/sts.* /scratch/local/sofia/db/\n");
print $name ("cp /uufs/sequence/sys/pkg/blast_db/std/est.* /scratch/local/sofia/db/\n");
print $name ("cp /uufs/sequence/sys/pkg/blast_db/std/gss.* /scratch/local/sofia/db/\n");
print $name ("cp /uufs/sequence/sys/pkg/blast_db/std/htgs.* /scratch/local/sofia/db/\n");
}
$x = 1;
#
# Loop through input sequence file name in the file searchlist.in and generate
# the actual part of the PBS scripts that does the searches
#
foreach $line (@line) {
  $name = "$ENV{HOME}/$direct/SCRIPT-$x";
  if ($line =~ m#x#)
    {print $name ("\"$BLAST_CLI_HOME/blastall -a 2 -p blastx -e 1 -b 5 -v 5 -d \$BLAST_DB/nr -i ..$line -o $line.htm -T T \n");
     if ($flag eq 2)
       {print $name ("perl /uufs/sequence/sys/pkg/blast/tblast_single.pl $line\n");
        print $name ("cd TBLASTX\n");
        $line =~ s#x##;
        print $name ("\"$BLAST_CLI_HOME/blastall -a 2 -p tblastx -e 1 -b 5 -v 5 -d \"\$BLAST_DB/nt
\$BLAST_DB/sts \$BLAST_DB/est \$BLAST_DB/gss \$BLAST_DB/htgs\" -i ..$line -o $line.htm -T T \n");
        print $name ("cd ..\n");
       }
     }
  if ($line =~ m#n#)
    {print $name ("\"$BLAST_CLI_HOME/blastall -a 2 -p blastn -e 1 -b 5 -v 5 -d \"\$BLAST_DB/nt
\$BLAST_DB/sts \$BLAST_DB/est \$BLAST_DB/gss \$BLAST_DB/htgs\" -i ..$line -o $line.htm -T T \n");
     $x++;
    if ($x > $nodes)
      { $x = 1; }
  }
#
#submit search jobs
#
foreach (1..$nodes){
  $name = "$ENV{HOME}/$direct/SCRIPT-$_";
  close ($name, ">$name");
  qx(qsub $name);
}
#
# Print message to user that scripts have been successfully submitted
#
  print "All batch jobs have been submitted. Check periodically by logging into sequence and doing a showq. Output
  files will be found in $ENV{HOME}/$direct/$YEARS-$MONTH-$DAY for the first stage search and
  $ENV{HOME}/$direct/$YEARS-$MONTH-$DAY/TBLASTX for the second stage search\n";

```

FIG. 14 (Cont'd)

```

#First get date of current database and store in date_db
#
qx(1n -s /uufs/sequence/sys/pkg/blast/std/.ncbirc .ncbirc);
$date_db = qx(/uufs/sequence/sys/pkg/blast/std/fastacmd -d /uufs/sequence/sys/pkg/blast_db/std/nr -I|grep Date|
cut -d " " -f5,6,7);

# Turn date_db into something useful
#
($m, $d, $y) = split(/ .?/, $date_db);
if ($m eq 'Jan') {
    $month = '01';
}
if ($m eq 'Feb') {
    $month = '02';
}
if ($m eq 'Mar') {
    $month = '03';
}
if ($m eq 'Apr') {
    $month = '04';
}
if ($m eq 'May') {
    $month = '05';
}
if ($m eq 'Jun') {
    $month = '06';
}
if ($m eq 'Jul') {
    $month = '07';
}
if ($m eq 'Aug') {
    $month = '08';
}
if ($m eq 'Sep') {
    $month = '09';
}
if ($m eq 'Oct') {
    $month = '10';
}

```

```

if ($m eq 'Nov')
  {$month = '11';}
if ($m eq 'Dec')
  {$month = '12';}

$d =~ s/.//;
if ($d < 10)
  {$d = '0' . $d}

chomp ($y);

$date_db_useful = "$y-$month-$d";
# get date of database used in last search and store in date_last
# parse date format to find newest directory

#@files is a list of all files in the search directory
#@dirs is a list of only the date directories in that search directory
# @files = qx(ls #ENV{HOME}/$direct);
foreach (@files)
  {chomp;}
foreach (@files)
  {
    if (m#\d+-\d+-\d+#+)
      {push @dirs, $_;}
  }
# find the greatest string in @dirs

```

```
#PBS -S /bin/csh
#PBS -q sequence
#PBS -W qos=2
#PBS -l walltime=222:00:00, nodes=1:ppn=2
#PBS -N Blast2
#PBS -e blast2.stderr
#PBS -o blast2.stdout
#
# set all environment variables needed
#
setenv BLAST_CLI_HOME /uufs/sequence/sys/pkg/blast/std
setenv BLAST_DB /scratch/local/sofia/db
setenv WORKDIR $HOME/seq_dev_2/search
#
# move to proper directory
#
cd $WORKDIR/2003-07-16
#
# link needed so Blast works
#
ln -s $BLAST_CLI_HOME/.ncbirc .ncbirc
#
# Clean up local scratch from last run and get local copy of all
# necessary databases
#
rm -r /scratch/local/sofia/db
mkdir -p /scratch/local/sofia/db
cp /uufs/sequence/sys/pkg/blast_db/std/nr.* /scratch/local/sofia/db
cp /uufs/sequence/sys/pkg/blast_db/std/nt.* /scratch/local/sofia/db
```

FIG. 15A

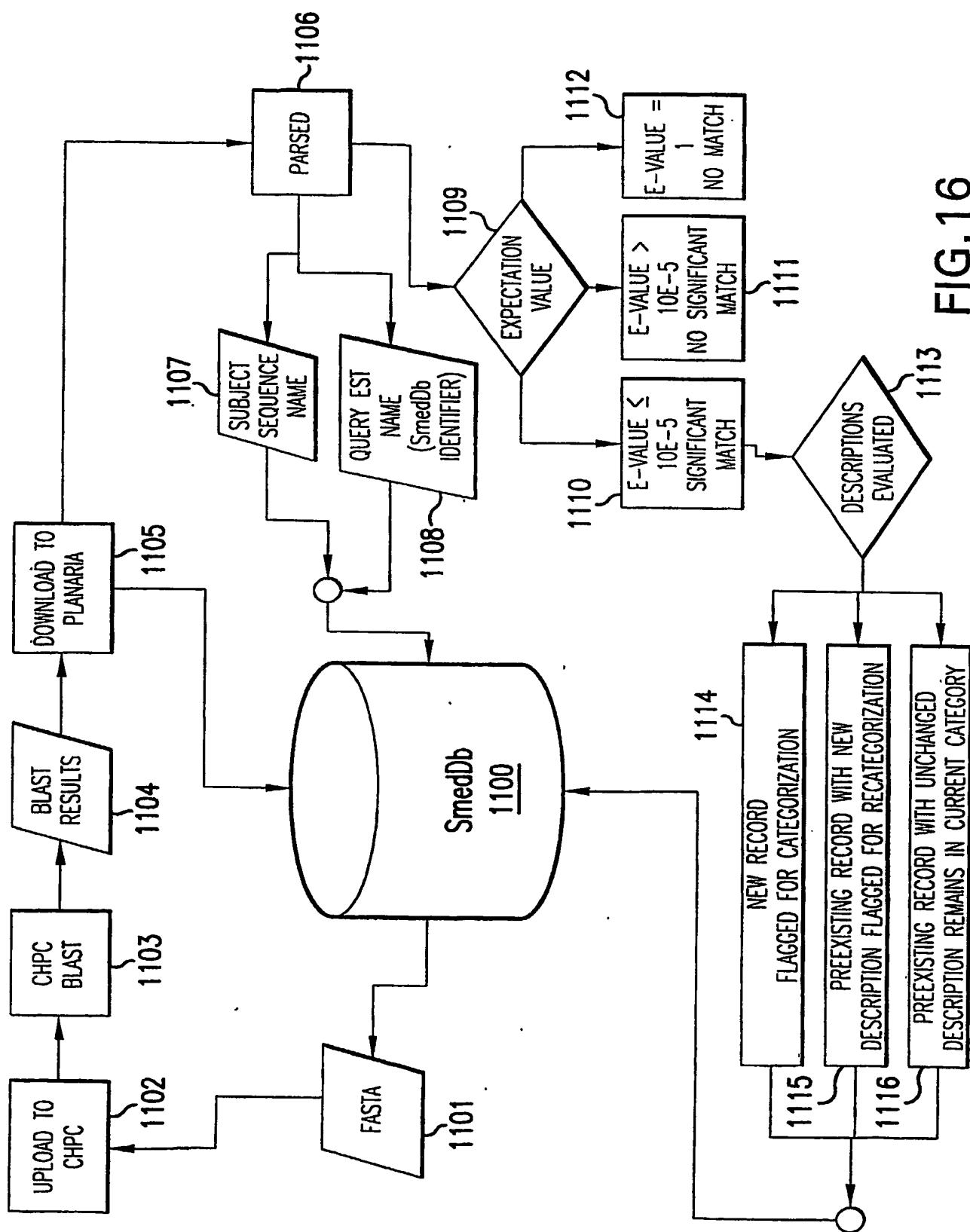
```

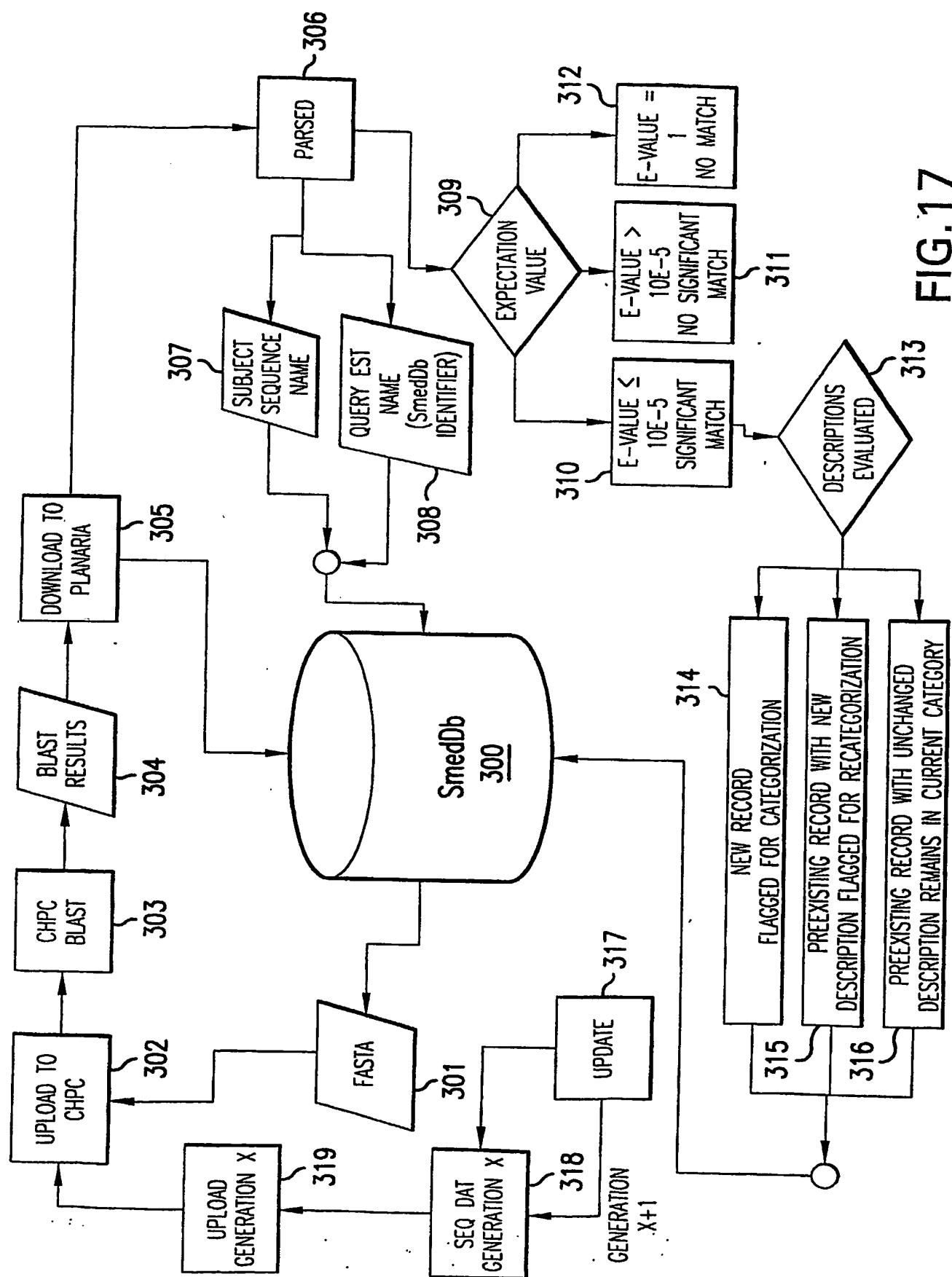
cp /uufs/sequence/sys/pkg/blast_db/std/sts.* /scratch/local/sofia/db.
cp /uufs/sequence/sys/pkg/blast_db/std/est.* /scratch/local/sofia/db.
cp /uufs/sequence/sys/pkg/blast_db/std/gss.* /scratch/local/sofia/db.
cp /uufs/sequence/sys/pkg/blast_db/std/htgs.* /scratch/local/sofia/db.

# The rest of the script runs the searches for the given input files (2x12, 9x12, and 16x12 shown)
# This particular script does both the first and second stage searches on each file;
# between the two stages the output of the first stage is parsed to check for searches
# in which "No hits found"; for these searches the second stage input files are then created.

# $BLAST_CLI_HOME/blastall -a 2 -p blastx -e 1 -b 5 -v 5 -d $BLAST_DB/nr -i ./2x12 -o 2x12.htm -T T
perl /uufs/sequence/sys/blast/tblast_single.pl 2x12
cd TBLASTX
$BLAST_CLI_HOME/blastall -a 2 -p blastx -e 1 -b 5 -v 5 -d "$BLAST_DB/nt $BLAST_DB/sts $BLAST_DB/est
$BLAST_DB/gss $BLAST_DB/htgs" -i ./2x12 -o 2x12.htm -T T
cd ..
$BLAST_CLI_HOME/blastall -a 2 -p blastx -e 1 -b 5 -v 5 -d $BLAST_DB/nr -i ./9x12 -o 9x12.htm -T T
perl /uufs/sequence/sys/blast/tblast_single.pl 9x12
cd TBLASTX
$BLAST_CLI_HOME/blastall -a 2 -p blastx -e 1 -b 5 -v 5 -d "$BLAST_DB/nt $BLAST_DB/sts $BLAST_DB/est
$BLAST_DB/gss $BLAST_DB/htgs" -i ./9x12 -o 9x12.htm -T T
cd ..
$BLAST_CLI_HOME/blastall -a 2 -p blastx -e 1 -b 5 -v 5 -d $BLAST_DB/nr -i ./16x12 -o 16x12.htm -T T
perl /uufs/sequence/sys/blast/tblast_single.pl 16x12
cd TBLASTX
$BLAST_CLI_HOME/blastall -a 2 -p blastx -e 1 -b 5 -v 5 -d "$BLAST_DB/nt $BLAST_DB/sts $BLAST_DB/est
$BLAST_DB/gss $BLAST_DB/htgs" -i ./16x12 -o 16x12.htm -T T
cd ..

```





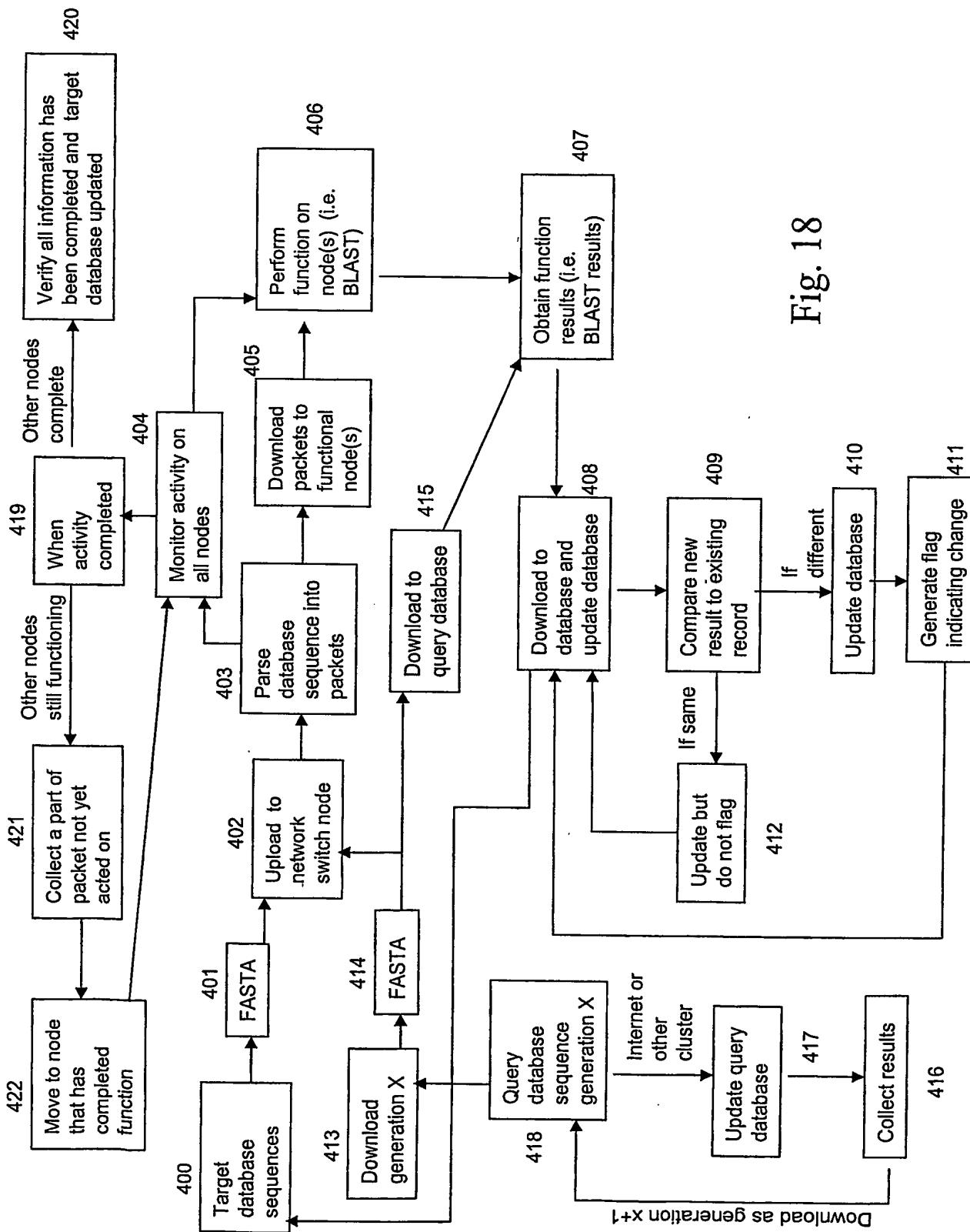


Fig. 18

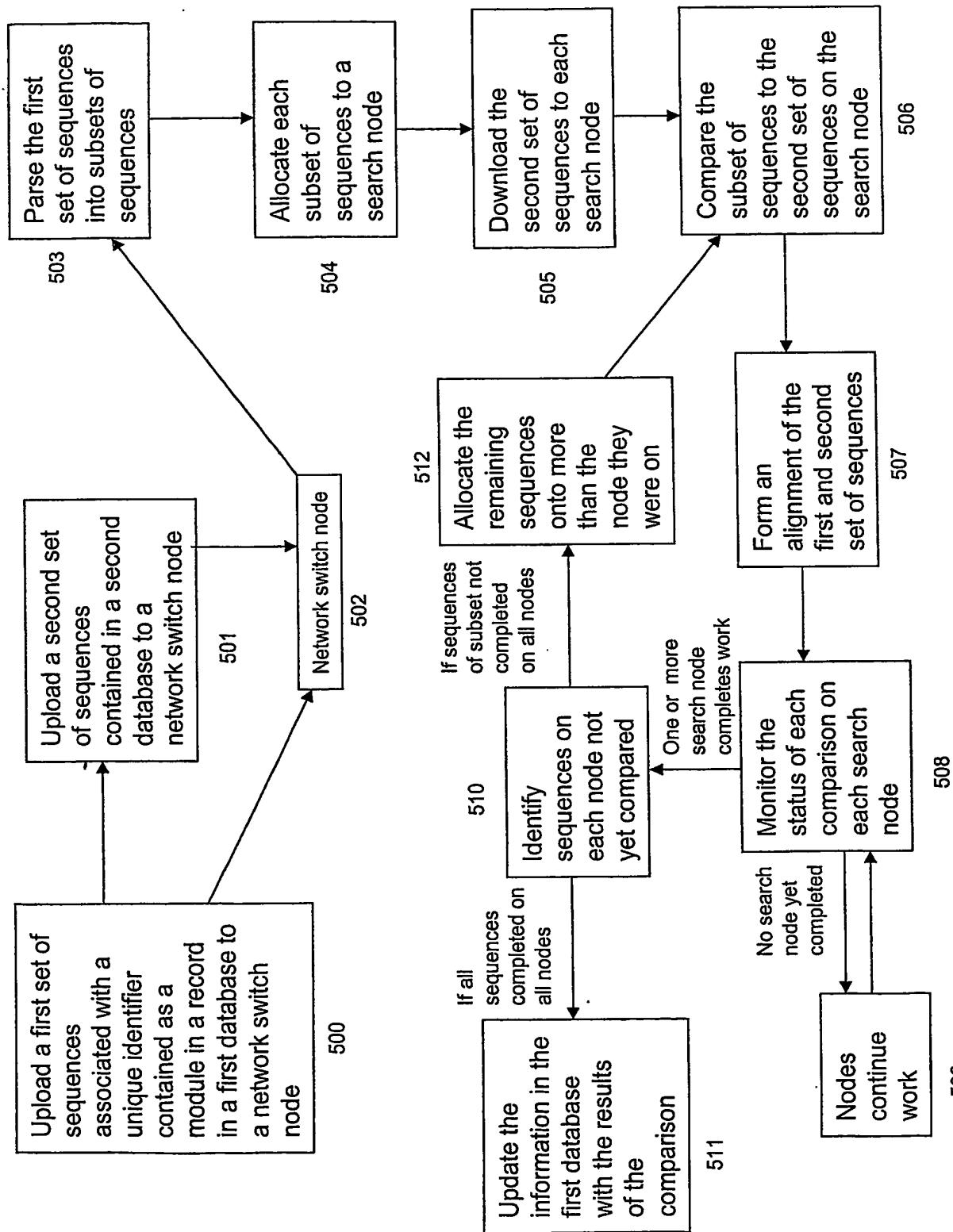


Fig. 19

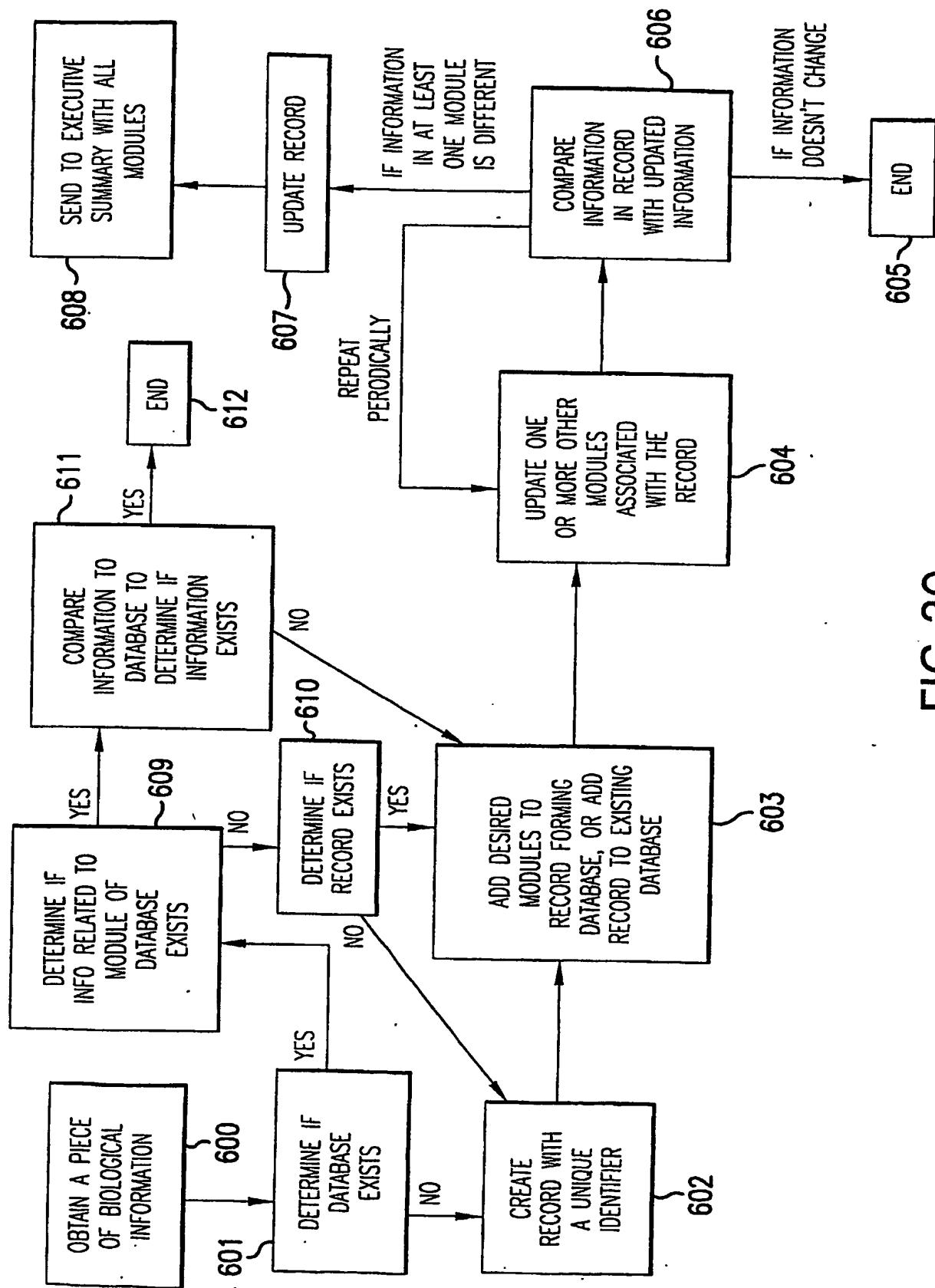


FIG. 20

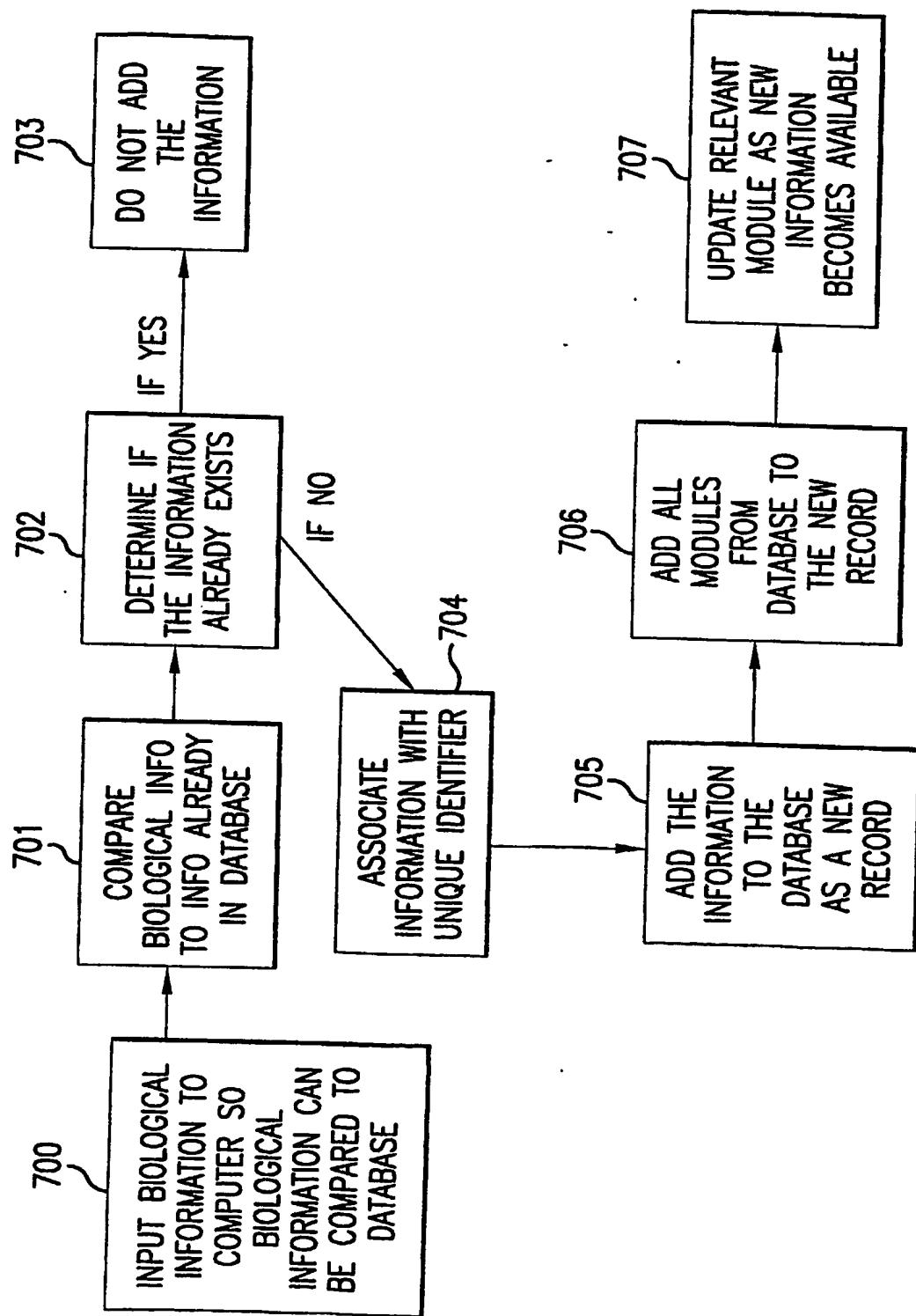


FIG.21

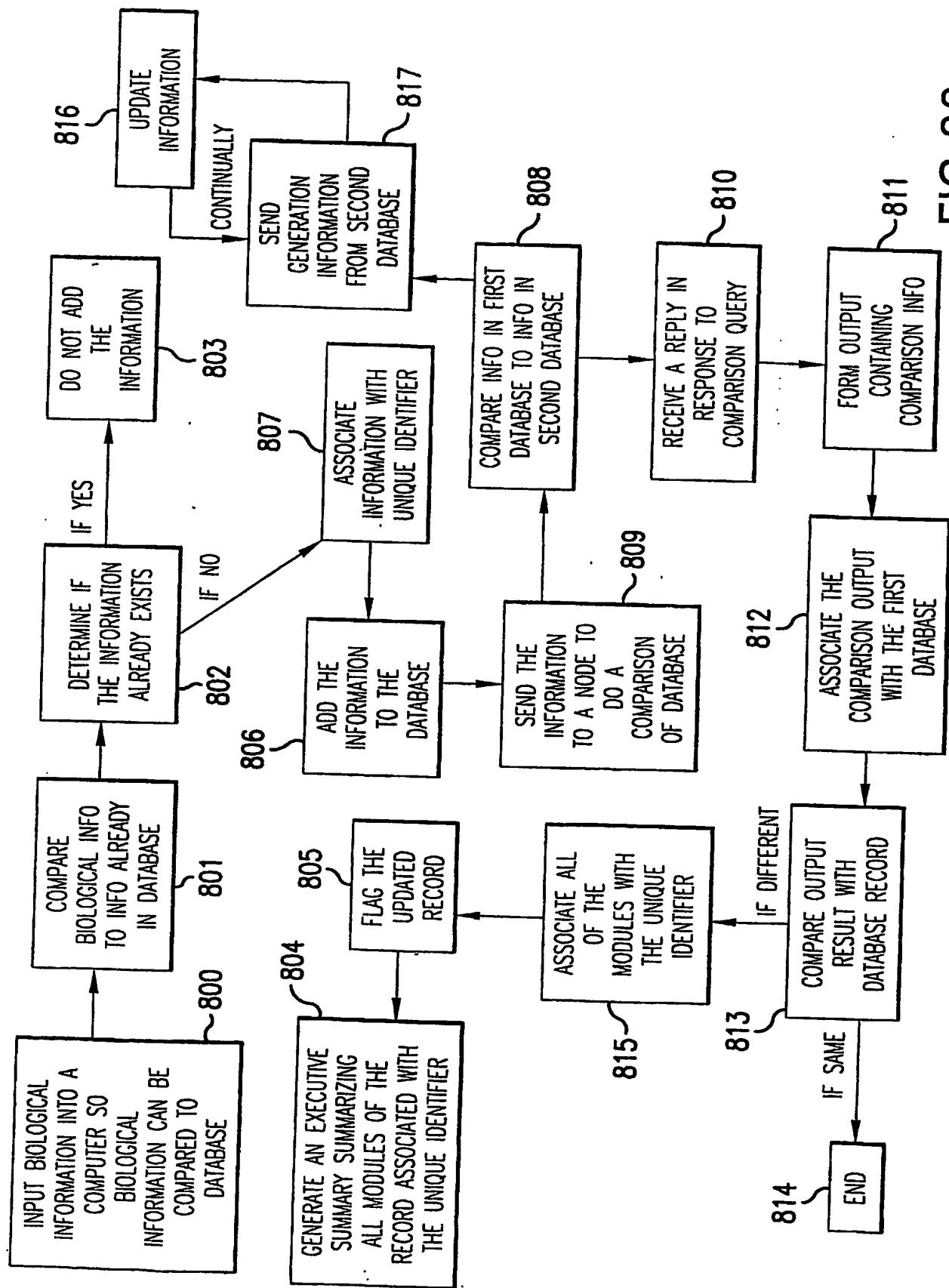


FIG. 22

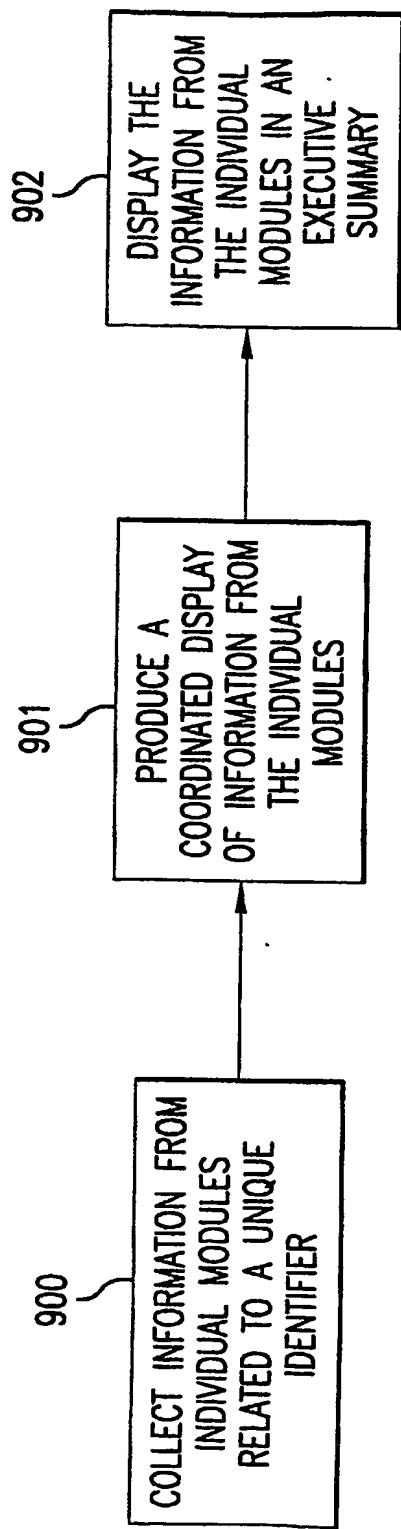


FIG. 23

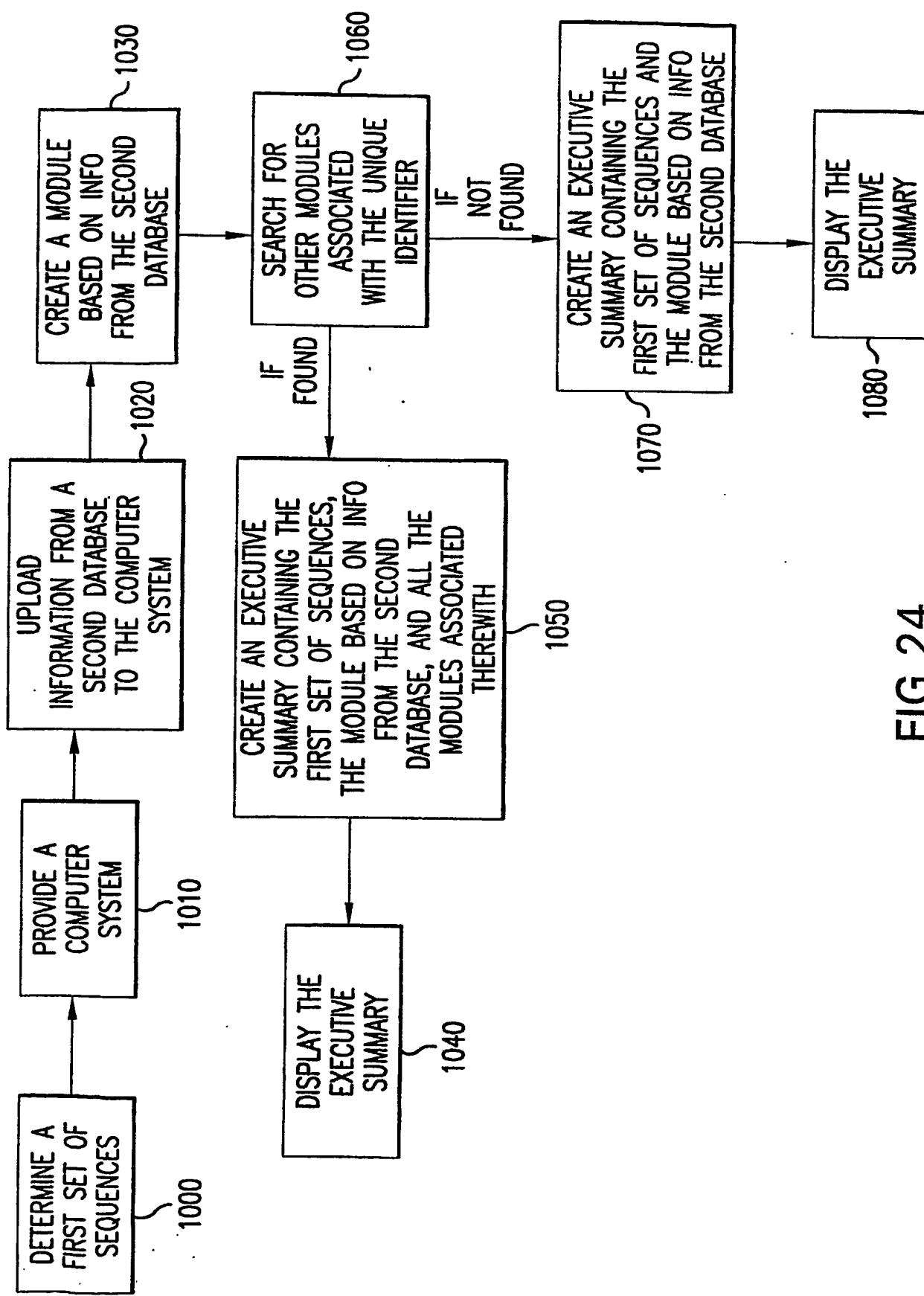


FIG.24